WHAT IS CLAIMED IS:

1. A genomic DNA library maintaining substantially copy numbers of a set of genes or sequences on a genomic DNA and an abundance ratio of said set of genes or sequences on the genomic DNA.

2. The genomic DNA library according to claim 1, which is obtained by carrying out a process comprising the steps of

(1) subjecting a genomic DNA to DNA fragmentation means for generating a mixture of fragmented DNAs having distribution ratio of 1 to 5 as defined by the size ratio (distribution ratio) of the maximum size of fragmented DNA to the minimum size of fragmented DNA and having a size convergence rate of 80% or more, thereby giving a mixture of fragmented DNAs; and

(2) subjecting the mixture of fragmented DNAs obtained in step (1) to nucleic acid amplification, thereby producing DNAs corresponding to said mixture of fragmented DNAs.

3. The genomic DNA library according to claim 2, wherein said mixture of fragmented DNAs obtained in step (1) is a mixture of DNAs having distribution ratio of 1 to 5 as defined by the size ratio (distribution ratio) of the maximum size of fragmented DNA to the minimum size of fragmented DNA.

4. The genomic DNA library according to claim 2, wherein said mixture of fragmented DNAs obtained in step (1) is a mixture of DNAs having a size convergence rate of 80% or more.

5. The genomic DNA library according to claim 2, wherein said mixture of fragmented DNAs obtained in step (1) is a mixture of DNAs having an average size of from 0.8 kbp to 1.5 kbp.

6. The genomic DNA library according to claim 2, wherein said nucleic acid amplification is Polymerase Chain Reaction (PCR) method.

7. A method for producing a genomic DNA library, comprising the steps of

(1) subjecting a genomic DNA to DNA fragmentation means for generating a mixture of fragmented DNAs having distribution ratio of 1 to 5 as defined by the size ratio (distribution ratio) of the maximum size of fragmented DNA to the minimum size of fragmented DNA and having a size convergence rate of 80% or more, thereby giving a mixture of fragmented DNAs; and

(2) subjecting the mixture of fragmented DNAs obtained in step (1) to nucleic acid amplification, thereby producing DNAs corresponding to said mixture of fragmented DNAs, to give a genomic DNA library maintaining substantially copy numbers of a set of genes or sequences on a genomic DNA and an abundance ratio of said set of genes or sequences on the genomic DNA.

8. The method according to claim 7, wherein said DNA fragmentation means is physical means.

9. The method according to claim 8, wherein said physical means is hydrodynamic point-sink shearing method.

10. The method according to claim 7, wherein said mixture of fragmented DNAs is a mixture of DNAs having distribution ratio of 1 to 5 as defined by the size ratio (distribution ratio) of the maximum size of fragmented DNA to the minimum size of fragmented DNA.

11. The method according to claim 7, wherein said mixture of fragmented DNAs is a mixture of DNAs having a size convergence rate of 80% or more.

12. The method according to claim 7, wherein said mixture of fragmented DNAs is a mixture of DNAs having an average size of from 0.8 kbp to 1.5 kbp.

13. The method according to claim 7, comprising the steps of:

(a) subjecting a genomic DNA to said DNA fragmentation means, thereby giving fragmented DNAs;

(b) ligating adapter DNA to the fragmented DNAs obtained in step (a), thereby giving DNA fragments; and

(c) carrying out nucleic acid amplification using the DNA fragments obtained in step (b) as a template and amplification primers, to give a genomic DNA library.

14. The method according to claim 13, wherein said DNA fragmentation means in step (a) is hydrodynamic point-sink shearing method.

15. The method according to claim 13, wherein said nucleic acid amplification in step (c) is Polymerase Chain Reaction (PCR) method.

16. The method according to claim 13, wherein said amplification primers used in the nucleic acid amplification in step (c) are primers selected from the group consisting of:

(i) oligonucleotides having a sequence complementary to said adapter DNA, and

(ii) oligonucleotides further comprising recognition sequences for restriction endonucleases, linker sequences and promoter sequence for RNA polymerase, in the sequence of the oligonucleotides of the above item (i).

17. The method according to claim 13, wherein the nucleic acid amplification in step (c) is carried out by using a DNA polymerase having a proofreading activity.

18. The method according to claim 17, wherein said DNA polymerase is a thermostable DNA polymerase.

19. The method according to claim 17, wherein said DNA polymerase is a mixture of a DNA polymerase having 3'→5' exonuclease activity and a DNA polymerase having no 3'→5' exonuclease activity.

20. The method according to claim 17, wherein said DNA polymerase is a mixture of at least two kinds of DNA polymerases, each having 3'→5' exonuclease activity.

21. The method according to claim 17, wherein said DNA polymerase is a

mixture of α type DNA polymerase and non-α, non-pol I type DNA polymerase.

22. A kit for producing a genomic DNA library, comprising the following amplification reagents (1) to (6):

(1) DNA ligase,

(2) enzymes for blunting a terminal of DNA,

(3) thermostable DNA polymerase,

(4) adapter DNA,

(5) reagents for PCR, and

(6) amplification primers selected from the group consisting of:

(i) oligonucleotides each having a sequence complementary to said adapter DNA, and

(ii) oligonucleotides further comprising at least one selected from the group consisting of recognition sequences for restriction endonucleases, linker sequences and promoter sequence for RNA polymerase, in the sequence of the oligonucleotides of the above item (i), and

comprising an instruction manual showing a procedure for carrying out the method of claim 7 by using said amplification reagents,

wherein the kit is used for production of the genomic DNA library of any one of claims 1 to 6.